

19B  
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6-5-02

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## SEQUENCE LISTING

<110> Prayaga, Suhhirdas K  
Shimkets, Richard A

<120> Novel Polypeptides and Polynucleotides Encoding Same

<130> 15966-615

<140> 09/782,436  
<141> 2000-12-07

<150> 60/169,887  
<151> 1999-12-09

<150> 60/170,230  
<151> 1999-12-10

<160> 26

<170> PatentIn Ver. 2.1

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cagcctcttt ttacacaagg gctgtctga tgcttggaaat agggccttcc tggacaaaact 180  
ccagactgga tttcatcagc agctggaaaga cctggagacc tgctttggta tagaggatgg 240  
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gggagtacat ttcttcttga aagagaggaa attcaggaac tgtacctggg aggttgcgt 360  
aatggtaaag ggattttct taagcacaaa acttcaagaa aaagagaaca gaagaaaaga 420  
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<213> Homo sapiens

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Ser Leu Phe Cys Asp Leu Pro Lys Ala Gln Val Ile Ser Ala Leu His  
20 25 30

Lys Met His Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser  
35 40 45

Asp Ala Trp Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His  
50 55 60

Gln Gln Leu Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys

65                    70                    75                    80  
Gln Glu Ser Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg  
                      85                    90                    95  
Tyr Phe Gln Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn  
                      100                    105                    110  
Cys Thr Trp Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr  
                      115                    120                    125  
Lys Leu Gln Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn  
                      130                    135                    140  
Leu Glu Lys Val Ile Tyr Leu Ala Glu Glu  
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nnnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 180  
nnnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnna agctcaagggtg atttctgccccc tccataagat 240  
gcaccagcag atcttcagcc tcttttaca caaggccttgc tctgatgctt ggaataggc 300  
cttcctggac aaactccaga ctggatttca tcagcaagctg gaagacctgg agacctgctt 360  
tggtagatag gatggaaagc aagagtctgc cctggaaattt gagggcccta cactggccat 420  
aaagaggtac ttccaggggag tacatttctt cttggaaagag aggaaattca ggaactgtac 480  
ctgggagggtt gtcgtaatgg taaagggtt tttcttaagc acaaaaacttc aagaaaaaaga 540  
gaacagaaga aaagagaact gaaaaaaaaa tctggaaaag gtaatctatt tagcagaaga 600  
gtgaaagctg 610

*Sub C1  
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<223> Wherein Xaa is any amino acid.

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20

25

30

Xaa  
35 40 45

Xaa  
50 55 60

Xaa Xaa Xaa Xaa Lys Ala Gln Val Ile Ser Ala Leu His Lys Met His  
65 70 75 80

Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser Asp Ala Trp  
85 90 95

Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His Gln Gln Leu  
100 105 110

Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys Gln Glu Ser  
115 120 125

Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg Tyr Phe Gln  
130 135 140

Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn Cys Thr Trp  
145 150 155 160

Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr Lys Leu Gln  
165 170 175

Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn Leu Glu Lys  
180 185 190

Val Ile Tyr Leu Ala Glu Glu  
195

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gcagccgagc tgccgctggc agacaacttc atgcctccg tgccgcggcc cgacctggcc 240  
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ggcgccttcg ccgacctgctg ggcctgcgt gccctgcacc tggatggcaa ccggctgacc 360  
tcactggcg agggccagct gcgcggcctg gtcaacttgc gccacctcat cctcagcaac 420  
aaccagctgg cagcgctggc ggcggcgcc ctggatgatt gtgccgagac actggaggac 480  
ctcgacctct cctacaacaa cctcgagcag ctgcctggg aggccctggg ccgcctggc 540  
aacgtcaaca cgttgggcct cgaccacaac ctgctggctt ctgtgcccgc cggcgcttt 600  
tcccgcctgc acaagctggc ccggctggac atgacctcca accgcctgac cacaatccca 660  
cccgacccac tcttctcccg cctgccccctg ctgcgcaggc cccggggctc gcccgcctct 720  
gccctggtgc tggcctttgg cggaaacccc ctgcactgca actgcgagct ggtgtggctg 780  
cgtcgcctgg cgcgggagga cgacctcgag gcctgcgcgt ccccacctgc tctggcgcc 840  
cgctacttct gggcggtggg cgaggaggag tttgtctgctg agccgcggct ggtgactcac 900

cgctcaccac ctctggctgt gcccgcaggt cggccggctg ccctgcgctg ccgggcagtg 960  
 ggggacccag agccccgtgt gcgttgggtg tcaccccagg gccggctgct aggcaactca 1020  
 agccgtgccc gcgccttccc caatgggacg ctggagctgc tggtcaccga gccgggtgat 1080  
 ggtggcatct tcacctgcat tgccgccaat gcagctggcg aggccacagc tgctgtggag 1140  
 ctgactgtgg gtcccccacc accctcctcag ctgcacaaca gcaccagctg tgacccccc 1200  
 cgggacgggg atcctgatgc tctcacccta ccctccgctg cctctgcttc tgccaaagg 1260  
 gccgacactg ggccccctac cgaccgtggc gtccaggtga ctgagcacgg ggccacagct 1320  
 gctttgtcc agtggccgga tcagggcct atccggca tccgcatgta ccagatccag 1380  
 tacaacagct cggctgatga catcctcgta tacaggatga tcccgccgga gagccgctcg 1440  
 ttccctgctga cggacctggc gtcaggccgg acctacgatc tgtgcgtgtc cgccgtgtat 1500  
 gaggacagcg ccacggggct cacggccacg cggcctgtgg gtcgcggccg cttctccacc 1560  
 gaacctgcgc tgccgcatg cggggcgcgg cacgctccct tccctggccgga cacgatgatc 1620  
 atcgcgtgg gcggcgtcat cgtagcctcg gtactggctc tcatcttcgt gctgetaatg 1680  
 cgctacaagg tgcacggccgg ccagcccccc ggcaaggcca agattcccgcc gcctgttagc 1740  
 agcgtttgtc cccagaccaa cggcgcctcg ggccccacgc ccacgcccgc cccgcccc 1800  
 cggagcccg cggcgtcag ggcccacacc gtggtccagc tggactgca gcccctgggg 1860  
 cccggccacg aacctgtggg accctag 1887

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 <212> PRT  
 <213> Homo sapiens

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| <400> 6 |     |     |     |     |     |     |     |     |     |     |     |     |     |      |     |
| Met     | Ala | Ile | Leu | Pro | Leu | Leu | Leu | Cys | Leu | Leu | Pro | Leu | Ala | Pro  | Ala |
| 1       |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |      |     |
| Ser     | Ser | Pro | Pro | Gln | Ser | Ala | Thr | Pro | Ser | Pro | Cys | Pro | Arg | .Arg | Cys |
|         |     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |      |     |
| Arg     | Cys | Gln | Thr | Gln | Ser | Leu | Pro | Leu | Ser | Val | Leu | Cys | Pro | Gly  | Ala |
|         |     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |      |     |
| Gly     | Leu | Leu | Phe | Val | Pro | Pro | Ser | Leu | Asp | Arg | Arg | Ala | Ala | Glu  | Leu |
|         |     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |      |     |
| Arg     | Leu | Ala | Asp | Asn | Phe | Ile | Ala | Ser | Val | Arg | Arg | Asp | Leu | Ala  |     |
|         |     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |      | 80  |
| Asn     | Met | Thr | Gly | Leu | Leu | His | Leu | Ser | Leu | Ser | Arg | Asn | Thr | Ile  | Arg |
|         |     |     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |      |     |
| His     | Val | Ala | Ala | Gly | Ala | Phe | Ala | Asp | Leu | Arg | Ala | Leu | Arg | Ala  | Leu |
|         |     |     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |      |     |
| His     | Leu | Asp | Gly | Asn | Arg | Leu | Thr | Ser | Leu | Gly | Glu | Gly | Gln | Leu  | Arg |
|         |     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |      |     |
| Gly     | Leu | Val | Asn | Leu | Arg | His | Leu | Ile | Leu | Ser | Asn | Asn | Gln | Leu  | Ala |
|         |     |     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |      |     |
| Ala     | Leu | Ala | Ala | Gly | Ala | Leu | Asp | Asp | Cys | Ala | Glu | Thr | Leu | Glu  | Asp |
|         |     |     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |      | 160 |
| Leu     | Asp | Leu | Ser | Tyr | Asn | Asn | Leu | Glu | Gln | Leu | Pro | Trp | Glu | Ala  | Leu |
|         |     |     |     |     | 165 |     |     |     | 170 |     |     |     | 175 |      |     |

Gly Arg Leu Gly Asn Val Asn Thr Leu Gly Leu Asp His Asn Leu Leu  
180 185 190

Ala Ser Val Pro Ala Gly Ala Phe Ser Arg Leu His Lys Leu Ala Arg  
195 200 205

Leu Asp Met Thr Ser Asn Arg Leu Thr Thr Ile Pro Pro Asp Pro Leu  
210 215 220

Phe Ser Arg Leu Pro Leu Leu Ala Arg Pro Arg Gly Ser Pro Ala Ser  
225 230 235 240

Ala Leu Val Leu Ala Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu  
245 250 255

Leu Val Trp Leu Arg Arg Leu Ala Arg Glu Asp Asp Leu Glu Ala Cys  
260 265 270

Ala Ser Pro Pro Ala Leu Gly Gly Arg Tyr Phe Trp Ala Val Gly Glu  
275 280 285

Glu Glu Phe Val Cys Glu Pro Pro Val Val Thr His Arg Ser Pro Pro  
290 295 300

Leu Ala Val Pro Ala Gly Arg Pro Ala Ala Leu Arg Cys Arg Ala Val  
305 310 315 320

Gly Asp Pro Glu Pro Arg Val Arg Trp Val Ser Pro Gln Gly Arg Leu  
325 330 335

Leu Gly Asn Ser Ser Arg Ala Arg Ala Phe Pro Asn Gly Thr Leu Glu  
340 345 350

Leu Leu Val Thr Glu Pro Gly Asp Gly Gly Ile Phe Thr Cys Ile Ala  
355 360 365

Ala Asn Ala Ala Gly Glu Ala Thr Ala Ala Val Glu Leu Thr Val Gly  
370 375 380

Pro Pro Pro Pro Gln Leu Ala Asn Ser Thr Ser Cys Asp Pro Pro  
385 390 395 400

Arg Asp Gly Asp Pro Asp Ala Leu Thr Pro Pro Ser Ala Ala Ser Ala  
405 410 415

Ser Ala Lys Val Ala Asp Thr Gly Pro Pro Thr Asp Arg Gly Val Gln  
420 425 430

Val Thr Glu His Gly Ala Thr Ala Ala Leu Val Gln Trp Pro Asp Gln  
435 440 445

Arg Pro Ile Pro Gly Ile Arg Met Tyr Gln Ile Gln Tyr Asn Ser Ser  
450 455 460

Ala Asp Asp Ile Leu Val Tyr Arg Met Ile Pro Ala Glu Ser Arg Ser  
465 470 475 480

Phe Leu Leu Thr Asp Leu Ala Ser Gly Arg Thr Tyr Asp Leu Cys Val  
                  485                     490                 495  
  
 Leu Ala Val Tyr Glu Asp Ser Ala Thr Gly Leu Thr Ala Thr Arg Pro  
                  500                     505                 510  
  
 Val Gly Cys Ala Arg Phe Ser Thr Glu Pro Ala Leu Arg Pro Cys Gly  
                  515                     520                 525  
  
 Ala Pro His Ala Pro Phe Leu Gly Gly Thr Met Ile Ile Ala Leu Gly  
                  530                     535                 540  
  
 Gly Val Ile Val Ala Ser Val Leu Val Phe Ile Phe Val Leu Leu Met  
                  545                     550                 555                 560  
  
 Arg Tyr Lys Val His Gly Gly Gln Pro Pro Gly Lys Ala Lys Ile Pro  
                  565                     570                 575  
  
 Ala Pro Val Ser Ser Val Cys Ser Gln Thr Asn Gly Ala Leu Gly Pro  
                  580                     585                 590  
  
 Thr Pro Thr Pro Ala Pro Pro Ala Pro Glu Pro Ala Ala Leu Arg Ala  
                  595                     600                 605  
  
 His Thr Val Val Gln Leu Asp Cys Glu Pro Trp Gly Pro Gly His Glu  
                  610                     615                 620  
  
 Pro Val Gly Pro  
                  625

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 <211> 802  
 <212> DNA  
 <213> Equus caballus

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 ttttccccat ggccttcctg ccctctctct tgacggccct ggtggtgtac gagttatggc 180  
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 gccctacact ggccgtgaag aggtacttcc gggggatcca tctctacctg aaagagaaga 600  
 aatacagtga ctgtgcctgg gagattgtcc gaatggaaat catgagatcc ttctttcat 660  
 cagcaaacct gcaaggaagg ttaagaatga aggatggaga cctgggctca ccttggaaatg 720  
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 <212> PRT

<213> Homo sapiens

<400> 8

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Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu  
20 25 30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser  
35 40 45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu  
50 55 60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu  
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu  
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg  
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser  
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe  
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu  
180 185 190

Gly Ser Ser  
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<210> 9

<211> 195

<212> PRT

<213> Equus caballus

<400> 9

Met Ala Phe Ser Val Ser Ser Leu Met Ala Leu Val Val Ile Ser Ser  
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20 25 30

Arg Lys Gln Glu Thr Leu Arg Val Leu His Gln Met Glu Thr Ile Ser  
35 40 45

Pro Pro Ser Cys Leu Lys His Arg Thr Asp Phe Arg Phe Pro Gln Glu  
50 55 60

Gln Leu Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Thr Ser Val Leu  
65 70 75 80

Gln Glu Met Leu Gln Gln Ile Val Ser Leu Phe His Thr Glu Arg Ser  
85 90 95

Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Arg Leu Leu Ala Gly Leu  
100 105 110

His Gln Gln Leu Glu Asp Leu Asn Thr Cys Leu Asp Glu Gln Thr Gly  
115 120 125

Glu Glu Glu Ser Ala Leu Gly Thr Val Gly Pro Thr Leu Ala Val Lys  
130 135 140

Arg Tyr Phe Arg Arg Ile Arg Leu Tyr Leu Thr Glu Lys Lys Tyr Ser  
145 150 155 160

Asp Cys Ala Trp Glu Ile Val Arg Val Asp Ile Met Arg Ser Phe Ser  
165 170 175

Ser Ser Ala Asn Leu Gln Gly Arg Leu Gly Met Lys Asp Gly Asp Leu  
180 185 190

Gly Ser Pro  
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<211> 117  
<212> PRT  
<213> Artificial Sequence

<220>  
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Domain 71-187

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Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn  
20 25 30

Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr  
35 40 45

Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu Ala Pro  
50 55 60

Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr  
65 70 75 80

Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys  
85 90 95

Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser  
100 105 110

Ser Thr Ala Leu Gln  
115

<210> 11  
<211> 194  
<212> PRT  
<213> Felis catus

<400> 11  
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Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu  
20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro  
35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp  
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val  
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser  
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly  
100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val  
115 120 125

Glu Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp  
130 135 140

Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu  
145 150 155 160

Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met  
165 170 175

Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser  
180 185 190

Glu Lys

<210> 12

<211> 195  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
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Gly Pro Gly Gly Ser Leu Gly Cys Asp Leu Ser Gln Asn His Val Leu  
   20              25              30

Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser  
   35              40              45

Pro His Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu  
   50              55              60

Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu  
   65              70              75              80

His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser  
   85              90              95

Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu  
   100             105             110

His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly  
   115             120             125

Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys  
   130             135             140

Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser  
   145             150             155             160

Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser  
   165             170             175

Ser Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu  
   180             185             190

Ser Ser Pro  
   195

<210> 13  
 <211> 195  
 <212> PRT  
 <213> Equus caballus

<400> 13  
 Met Ala Leu Leu Pro Ser Leu Leu Thr Ala Leu Val Val Tyr Glu Leu  
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Trp Pro Cys Gly Ala Leu Gly Cys Asp Leu Pro Gln Asn His Ile Leu  
   20              25              30

Val Ser Arg Lys Asn Phe Val Leu Leu Gly Gln Met Ser Arg Ile Ser  
                  35                 40                 45  
  
 Ser Ala Ile Cys Leu Lys Asp Arg Lys Asp Phe Arg Phe Pro Gln Asp  
      50                 55                 60  
  
 Met Ala Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Ala Ser Val Leu  
    65                 70                 75                 80  
  
 His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
    85                 90                 95  
  
 Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Glu Leu Cys Thr Gly Leu  
   100                 105                 110  
  
 Leu Arg Gln Leu Glu Asp Leu Asp Thr Cys Leu Glu Gln Glu Met Gly  
   115                 120                 125  
  
 Glu Glu Glu Ser Ala Leu Gly Thr Val Arg Pro Thr Leu Ala Val Lys  
   130                 135                 140  
  
 Arg Tyr Phe Arg Gly Ile His Leu Tyr Leu Lys Glu Lys Lys Tyr Ser  
   145                 150                 155                 160  
  
 Asp Cys Ala Trp Glu Ile Val Arg Met Glu Ile Met Arg Ser Phe Ser  
   165                 170                 175  
  
 Ser Ser Ala Asn Leu Gln Gly Arg Leu Arg Met Lys Asp Gly Asp Leu  
   180                 185                 190  
  
 Gly Ser Pro  
   195

<210> 14  
 <211> 195  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
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 Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu  
   20                 25                 30  
  
 Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser  
   35                 40                 45  
  
 Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu  
   50                 55                 60  
  
 Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu  
   65                 70                 75                 80  
  
 His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
   85                 90                 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu  
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg  
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser  
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe  
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu  
180 185 190

Gly Ser Ser  
195

<210> 15  
<211> 65  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Consensus  
sequence

<400> 15  
Ala Gln Ser Val Leu His Met Gln Gln Ile Phe Leu Phe Thr Glu Ser  
1 5 10 15

Ser Ala Ala Trp Asn Thr Leu Leu Thr Gly Leu Gln Leu Leu Cys Gln  
20 25 30

Gly Glu Glu Ser Ala Leu Pro Leu Arg Tyr Phe Gln Gly Tyr Leu Lys  
35 40 45

Glu Lys Tyr Ser Cys Ala Trp Glu Val Arg Glu Ile Met Ser Leu  
50 55 60

Gln  
65

<210> 16  
<211> 166  
<212> PRT  
<213> Homo sapiens

<400> 16  
Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln  
1 5 10 15

Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu  
     20                 25                 30

Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln  
     35                 40                 45

Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln  
     50                 55 ..         60

Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn  
     65                 70                 75                 80

Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn  
     85                 90                 95

His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr  
     100                105             110

Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg  
     115                120             125

Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr  
     130                135             140

Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu  
     145                150             155             160

Thr Gly Tyr Leu Arg Asn  
     165

<210> 17  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

<400> 17  
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
     1              5                 10                 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
     20             25                 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
     35             40                 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
     50             55                 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
     65             70                 75                 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
     85             90                 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Asn

| 100   | 105 | 110 |
|---|-----|-----|
| Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu |     |     |
| 115   | 120 | 125 |
| Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg |     |     |
| 130   | 135 | 140 |
| Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser |     |     |
| 145   | 150 | 155 |
| Leu Arg Ser Lys Glu   |     |     |
| 165   |     |     |

<210> 18  
 <211> 189  
 <212> PRT  
 <213> Mus musculus

|   |     |     |
|---|-----|-----|
| <400> 18  |     |     |
| Met Ala Arg Leu Cys Ala Phe Leu Met Val Leu Ala Val Met Ser Tyr |     |     |
| 1   | 5   | 10  |
| Trp Pro Thr Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Asn Leu |     |     |
| 20  | 25  | 30  |
| Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser |     |     |
| 35  | 40  | 45  |
| Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu |     |     |
| 50  | 55  | 60  |
| Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu |     |     |
| 65  | 70  | 75  |
| 80  |     |     |
| Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser |     |     |
| 85  | 90  | 95  |
| Ser Ala Ala Trp Asn Ala Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu |     |     |
| 100   | 105 | 110 |
| His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly |     |     |
| 115   | 120 | 125 |
| Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg |     |     |
| 130   | 135 | 140 |
| Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser |     |     |
| 145   | 150 | 155 |
| 160   |     |     |
| Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser |     |     |
| 165   | 170 | 175 |
| Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys             |     |     |
| 180   | 185 |     |

<210> 19  
<211> 195  
<212> PRT  
<213> Antilocapra americana

<400> 19  
Met Ala Gln Leu Leu Pro Leu Leu Thr Ala Leu Val Leu Cys Ser Tyr  
1 5 10 15  
  
Gly Pro Val Gly Ser Leu Gly Cys Asp Leu Pro His Asn Ser Ala Pro  
20 25 30  
  
Leu Ser Arg Lys Thr Leu Val Leu Leu Asp Gln Met Arg Arg Val Ser  
35 40 45  
  
Pro Val Leu Cys Leu Lys Asp Arg Arg Asp Phe Gln Phe Pro Arg Glu  
50 55 60  
  
Val Val Asn Gly Ser Gln Phe Gln Lys Asn Gln Thr Val Ser Val Leu  
65 70 75 80  
  
His Glu Met Leu Gln Gln Ile Phe Asn Leu Leu His Thr Ala Arg Ser  
85 90 95  
  
Ser Ala Ala Trp Asn Asn Thr Leu Leu Glu Glu Leu His Thr Ala Leu  
100 105 110  
  
His Gln Gln Leu Gln Gly Leu Glu Thr Cys Leu Val Gln Ala Met Gly  
115 120 125  
  
Glu Glu Asp Ser Val Leu Thr Ala Asp Ser Pro Met Leu Met Leu Lys  
130 135 140  
  
Arg Tyr Phe Gln Arg Ile Arg Leu Tyr Leu Asp Glu Lys Lys His Ser  
145 150 155 160  
  
Gly Cys Ala Trp Glu Leu Val Arg Met Glu Ile Arg Arg Ala Phe Ser  
165 170 175  
  
Ser Thr Ala Asp Leu Gln Glu Ser Leu Arg Ser Lys Asp Gly Asp Leu  
180 185 190  
  
Ala Ser Ser  
195

<210> 20  
<211> 43  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Consensus  
sequence

<400> 20

Phe Pro Glu Gln Lys Leu Glu Met Gln Gln Ile Phe Phe Ser Ser Ala  
1 5 10 15

Trp Asn Thr Leu Gln Gln Leu Leu Cys Gly Leu Leu Tyr Phe Arg Ile  
20 25 30

Tyr Leu Glu Lys Lys Ser Cys Ala Trp Glu Val  
35 40

<210> 21  
<211> 184  
<212> PRT  
<213> Equus caballus

<400> 21  
Met Ala Leu Pro Val Ser Leu Leu Met Ala Leu Val Val Leu Ser Cys  
1 5 10 15

His Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro His Thr His Ser Leu  
20 25 30

Gly Asn Thr Arg Val Leu Met Leu Leu Gly Gln Met Arg Arg Ile Ser  
35 40 45

Pro Phe Ser Cys Leu Lys Asp Arg Asn Asp Phe Gly Phe Pro Gln Glu  
50 55 60

Val Phe Asp Gly Asn Gln Phe Arg Lys Pro Gln Ala Ile Ser Ala Val  
65 70 75 80

His Glu Thr Ile Gln Gln Ile Phe His Leu Phe Ser Thr Asp Gly Ser  
85 90 95

Ser Ala Ala Trp Asp Glu Ser Leu Leu Asp Lys Leu Tyr Thr Gly Leu  
100 105 110

Tyr Gln Gln Leu Thr Glu Leu Glu Ala Cys Leu Ser Gln Glu Val Gly  
115 120 125

Val Glu Glu Thr Pro Leu Met Asn Glu Asp Ser Leu Leu Ala Val Arg  
130 135 140

Arg Tyr Phe Gln Arg Ile Ala Leu Tyr Leu Gln Glu Lys Lys Tyr Ser  
145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Phe Ser  
165 170 175

Ser Ser Thr Asn Leu Pro Gln Ser  
180

<210> 22  
<211> 92  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Consensus sequence

<400> 22

Ser Leu Leu Ala Leu Val Ser Leu Gly Cys Asp Leu Pro His Leu Leu  
1 5 10 15

Leu Gln Met Arg Cys Lys Asp Arg Asp Phe Phe Pro Gln Gly Gln Lys  
20 25 30

Ala Gln Ser His Gln Gln Ile Phe Leu Phe Thr Ser Ser Ala Ala Trp  
35 40 45

Asn Leu Leu Asp Leu Thr Gly Leu Gln Leu Leu Glu Cys Gln Glu Gly  
50 55 60

Glu Leu Leu Arg Tyr Phe Gln Tyr Leu Glu Lys Lys Tyr Ser Cys Ala  
65 70 75 80

Trp Glu Val Arg Glu Ile Met Ser Ser Thr Leu Gln  
85 90

<210> 23

<211> 3144

<212> DNA

<213> Homo sapiens

<400> 23

gcctggctcc ctctcgctga gacacacata cactcacaca tacacaaccc ggcaggctcg 60  
tctgaacttg aagacacccc acattccaag atgcccagg ttcctggaa tgcctgggt 120  
tcttcgatcc ggaaaatctt accggcatcc tccttagggag ggattattat tattatttt 180  
ctttaatctg gaagagaaga gaacaagttg tgctttccc cccttcttct tgctaaacgc 240  
catggatata actgaataag cggtctcaggg ctttccccgc gtggacgtcc gaggccacca 300  
tctgcctgca ttgcggag ccggcggagg gtttagctcg agtctgtctc gggcggggaa 360  
ggatgcgtgg ccgagccggg gagcccgggc gccccgsgga gccggcctcg gtgccaccca 420  
gccgggggta gatgctgcct cgcccaggcg ctgagtgacc agaccatgga gaccctgctt 480  
ggtggcctgc tagcggttgg catggcgttt gccgtgtcg acgcctgccc caagtactgt 540  
gtctgccaga atctgtctga gtcactgggg accctgtgcc cctccaaggg gctgctctt 600  
gtaccccttg atattgaccg gcggacagtg gagctgcgcc tggcggcaa cttcatcatc 660  
cacatcagcc gccaggactt tgccaacatg acggggctgg tggacctgac cctgtccagg 720  
aacaccatca gccacatcca gccctttcc tttctggacc tcgagagcct ccgctccctg 780  
catcttgaca gcaatcggt gccaagcctt ggggaggaca ccctccgggg cctggtaaac 840  
ctgcagcacc ttatcgtaa caacaaccag ctggcggca tcgcagatga ggctttgag 900  
gacttcctgc tgacatttggaa ggatctggac ctctcctaca acaacctcca tggcctgccc 960  
tgggactccg tgcgacgcac ggtcaacctc caccagctga gcttggacca caacctgtcg 1020  
gatcacatcg ccgaggccac ctttgcagac ctgcagaaac tgcccgccct ggatctcacc 1080  
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tgcaatttgt agcttctcg gtcgaggagg ctgcagccgg acatgacact ggaaacctgt 1260  
ggctccccag ggggcctcaa gggtcgctac ttctggcatg tgcgtgagga ggagttgtg 1320  
tgcgagccgc ctctcatcac ccacgcacaca cacaaggctgc tggttctgga gggccaggcg 1380  
gccacactca agtgcaaagc cattggggac cccagccccc ttatccactg ggtagccccc 1440  
gatgaccgccc tggtagggaa ctcctcaagg accgctgtct atgacaatgg caccctggac 1500  
atcttcatca ccacatctca ggacagtggc gccttcaccc gtattgtcgcaatgtcgcc 1560

ggagaggcca cggccatggt ggaggtctcc atcgccacgc tgccacaccc cagcaacacgc 1620  
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 agccggggag gtggaggcag tggggccga gagcctccca aaagcccccc ggaacgggct 1740  
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 tacaggatga tcccagcctc caacaaggcc ttcgtggta acaacctggt gtcagggact 1920  
 ggctacgact tgggtgtgct ggccatgtgg gatgacacag ccacgacact cacggccacc 1980  
 aacatcgtgg gctgcgecca gttttcacc aaggctgact acccgcagtg ccagttcatg 2040  
 cacagccaga ttctggccgg caccatgatc ctggtcatcg ggggcatcat cgtggccacg 2100  
 ctgctggctc tcatacgcat cctcatggt cgctacaagg tctgcaacca cgaggcccc 2160  
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 cctccaagca ggcgcaccagg cggggccccg ccgcagggcc cggcgaaggt ggtggcgc 2280  
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 gcaagcggct ttggattgtc tatg 3144

<210> 24  
 <211> 832  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
 Leu Glu Ser Val Ser Gly Gly Glu Gly Cys Val Ala Glu Pro Gly Ser  
 1 5 10 15

Pro Gly Ala Pro Arg Ser Arg Pro Arg Cys His Pro Ala Gly Gly Arg  
 20 25 30

Cys Cys Leu Ala Gln Ala Leu Ser Asp Gln Thr Met Glu Thr Leu Leu  
 35 40 45

Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala Cys  
 50 55 60

Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr Leu  
 65 70 75 80

Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg Arg  
 85 90 95

Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser Arg  
 100 105 110

Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser Arg

|   |     |     |
|---|-----|-----|
| 115   | 120 | 125 |
| Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu Ser |     |     |
| 130   | 135 | 140 |
| Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly Glu |     |     |
| 145   | 150 | 155 |
| Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn Asn |     |     |
| 165   | 170 | 175 |
| Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu Leu |     |     |
| 180   | 185 | 190 |
| Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu Pro |     |     |
| 195   | 200 | 205 |
| Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu Asp |     |     |
| 210   | 215 | 220 |
| His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu Gln |     |     |
| 225   | 230 | 235 |
| Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu Pro |     |     |
| 245   | 250 | 255 |
| Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala Thr |     |     |
| 260   | 265 | 270 |
| Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu His |     |     |
| 275   | 280 | 285 |
| Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp Asp |     |     |
| 290   | 295 | 300 |
| Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe Trp |     |     |
| 305   | 310 | 315 |
| His Val Arg Glu Glu Phe Val Cys Glu Pro Pro Leu Ile Thr Gln     |     |     |
| 325   | 330 | 335 |
| His Thr His Lys Leu Leu Val Leu Glu Gly Gln Ala Ala Thr Leu Lys |     |     |
| 340   | 345 | 350 |
| Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile His Trp Val Ala Pro |     |     |
| 355   | 360 | 365 |
| Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr Ala Val Tyr Asp Asn |     |     |
| 370   | 375 | 380 |
| Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln Asp Ser Gly Ala Phe |     |     |
| 385   | 390 | 395 |
| Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala Thr Ala Met Val Glu |     |     |
| 405   | 410 | 415 |
| Val Ser Ile Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg Thr |     |     |

|   |     |     |
|---|-----|-----|
| 420   | 425 | 430 |
| Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr Gly Ser Ser Lys Thr |     |     |
| 435   | 440 | 445 |
| Ser Arg Gly Gly Gly Ser Gly Gly Glu Pro Pro Lys Ser Pro         |     |     |
| 450   | 455 | 460 |
| Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr Thr Thr Ser Ala Leu |     |     |
| 465   | 470 | 475 |
| 480   |     |     |
| Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr Gln |     |     |
| 485   | 490 | 495 |
| Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu Ile Tyr Arg Met Ile |     |     |
| 500   | 505 | 510 |
| Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn Leu Val Ser Gly Thr |     |     |
| 515   | 520 | 525 |
| Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp Asp Thr Ala Thr Thr |     |     |
| 530   | 535 | 540 |
| Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln Phe Phe Thr Lys Ala |     |     |
| 545   | 550 | 555 |
| 560   |     |     |
| Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly Thr |     |     |
| 565   | 570 | 575 |
| Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala Thr Leu Leu Val Phe |     |     |
| 580   | 585 | 590 |
| Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala Pro |     |     |
| 595   | 600 | 605 |
| Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn Gly |     |     |
| 610   | 615 | 620 |
| Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala Pro Pro Gln |     |     |
| 625   | 630 | 635 |
| 640   |     |     |
| Gly Pro Pro Lys Val Val Arg Asn Glu Leu Leu Asp Phe Thr Ala     |     |     |
| 645   | 650 | 655 |
| Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Leu Gly Ser     |     |     |
| 660   | 665 | 670 |
| Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro Ser |     |     |
| 675   | 680 | 685 |
| Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe Ala |     |     |
| 690   | 695 | 700 |
| Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser Arg |     |     |
| 705   | 710 | 715 |
| 720   |     |     |
| Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His His Ser |     |     |

|   |     |     |
|---|-----|-----|
| 725   | 730 | 735 |
| Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg Ser Leu |     |     |
| 740   | 745 | 750 |
| Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser Phe Asp |     |     |
| 755   | 760 | 765 |
| Met Gly Asp Phe Ala Ala Ala Ala Gly Gly Val Val Pro Gly Gly     |     |     |
| 770   | 775 | 780 |
| Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg Ser Leu |     |     |
| 785   | 790 | 795 |
| Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val Gly |     |     |
| 805   | 810 | 815 |
| Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser Thr Val |     |     |
| 820   | 825 | 830 |

<210> 25  
<211> 98  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: IFAbd Domain  
13-110

<400> 25  
Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln  
1           5           10                           15  
              {  
Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn  
20           25                                   30

Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn  
35           40                                   45

His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr  
50           55                                   60

Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg  
65           70                                   75                           80

Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr  
85           90                                   95

Ile Val

<210> 26

<211> 183

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:pfam00143  
Domain 5-187

<400> 26

Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys Asn Ser Val Cys  
1 5 10 15

Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg  
20 25 30

Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys  
35 40 45

Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly  
50 55 60

Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn  
65 70 75 80

Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala  
85 90 95

Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln  
100 105 110

Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu  
115 120 125

Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg  
130 135 140

Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser  
145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr  
165 170 175

Tyr Ser Ser Thr Ala Leu Gln  
180